

Fig.1.

```

PstI
1  CAGGTGCAGCTGCAGGAGTCAGGGGAGGCTTGGTGCAGGCTGGGAGTCTCTGAAACTCTCCTGTGCAGCCTCTGGAACACACCTTCAGT
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
90 GTCCACGTCGAGCTCCTCAGTCCCTCCGAACCAACGTCGCCACCTCAGAGACTTTGAGAGGACACGTCGGAGACCTTTGTGGAAGTCA
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   Q V Q L Q E S G G L V Q A G E S L K L S C A A S G N T F S
   [-> CDR I

KpnI
91 GCGGCTTCATGGGCTGGTACCGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACCATTAATAGTAGAGGTATCACAAACTATGCA
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   CCGCCGAGTACCCGACCATGGCGGTCCGAGGTCCCTTCGTCGCGCTCAACCGCGTTGGTAATTATCATCTCCATAGTGTTCATACGT
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   G G F M G W Y R Q A P G K Q R E L V A T I N S R G I T N Y A
   [-> CDR II

EagI
181 GACTTCGTGAAGGCGGATTACCATCTCCAGAGACATGCCAAGAAGACAGTGTATTGGAAATGAACAGCCTGGAACTGAAGACACG
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   CTGAAGCACTTCCCGGCTAAGTGGTAGAGGTCTCTGTACGGTTCTTCTGTACATAAACCTTACTTTCGGACCTTGGACTTCGTGTC
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   D F V K G R F T I S R D N A K K T V Y L E M N S L E P E D T
   [-> CDR III

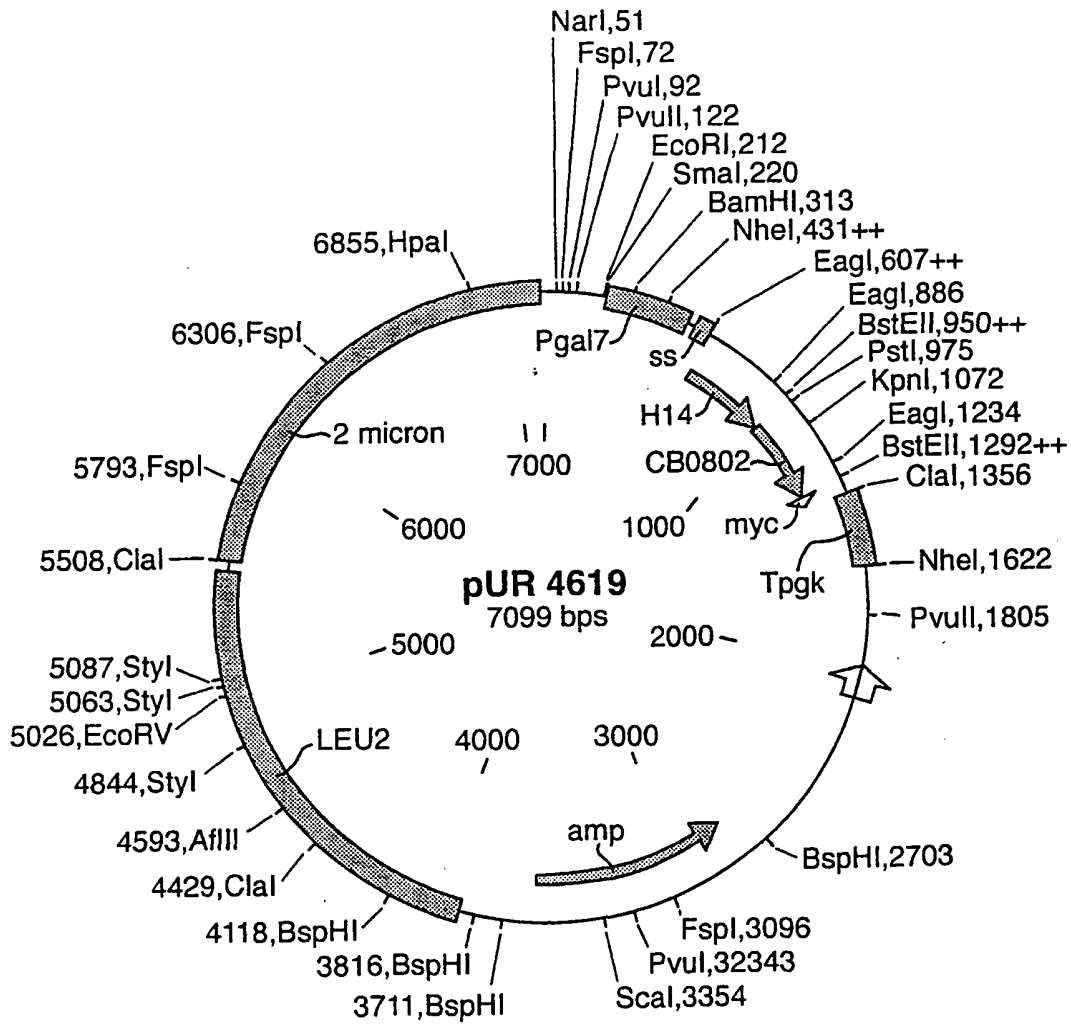
BstEII
271 GCCGTTTATTACTGTACACTCACTACTTCAGATCCTACTGGGTGAGGGGACCCAGGTCACCGTCTCCTCA
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   CGGCAATAATGACRATGTGAGTGATGAGTCTAGTAGTACCCCACTCCCTGGGTCCAGTGGCAGAGGAGT
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
   A V Y Y C Y T H Y F R S Y W G Q G T Q V T V S S
   [-> CDR III <->

```

**Pst I**

1  
CAGGTGCAGCTGCAGGAGTCAGGGGAGGATTGGTGCAGGCGGGGGGCTCTCTGAGACTCTCTCCTGTGCAGCCTCTGAGCAGCACCGGCAGT  
91  
GTCCACGTCGACGCTCCTCAGTCCCGCTCCTAACACAGTCGCGCCCGAGAGACTCTGAGAGGACACGTCGGAGACCTGCGTGGCCGTCA  
Q V Q L Q E S G G L V Q A G G S L R L S C A A S G R T G S  
91  
ACGTATGACATGGGCTGGTTCGCGCAGGCTCCAGGGAAGGAGCGTGAGTCTCTAGCAGCTATTAACTGSGATAGTGCAGGCACATACTAT  
181  
TGCATACTGTACCGACCAAGGCGGTCCGAGGTCCTTCTCGCACTCAGACATCGTCGATAATTGACCCCTATCACGGCGGTGTATGATA  
T Y D M G W F R Q A P G K E R E S V A A I N W D S A R T Y Y  
1-> CDR I <-1 1-> CDR II  
EagI  
GCAAGCTCCGTGAGGGCGGATTACCATCTCCAGAGACACGCCCAAGAGACGGTGTATCTGCAAAATGAACAGCCTGAAACCTGAGGAC  
181  
CGTTCGAGGCACTCCCGGCTAAGTGGTAGAGTCTCTGTTCGGTCTTCTGCCACATAGACGTTTACTTGTTCGACTTTGGACTCTCG  
A S S V R G R F T I S R D N A K K T V Y L Q M N S L K P E D  
<-1  
BstEII  
ACGGCCGTTTATACCTGTGGCGGGGGAAGTGGTACTTGGGACTCCTGGGGCCAGGGGACCCAGGTCACCGTCTCTCTCA  
271  
TGCCGGCAATATGGACACCGCGCCCTTCCACCATGAACCTGAGGACCCCGTCCCGTGGGTCCAGTGGCAGAGGAGT  
351  
T A V Y T C G A G E G T W D S W G Q G T Q V T V S S  
1-> CDR III <-1

Fig.3.



WO 00/24884

PCT/EP99/08323

4/7

Fig.4.

XhoI  
 1 CTCGAGTCAGGGGAGGATTGGTCAGCGGGGGGCTCTCTGAGACTCTCTGAGACCTCTGAGCCACCGGCAGTACGTATGACATG  
 90  
 GAGCTCAGTCCCCCTCCTAACCCAGCTCCGCCCCCGAGAGACTCTGAGAGGACACGTCGGAGACCTGGCTGGCCGTCATGCATACACTGTAC  
 L E S G G G L V Q A G G S L R L S C A A S G R T G S T Y D M  
 1-> CDR I  
 91 GGTGGTTCGCCAGGCTCCAGGAAGGAGCGTGAGTCTGTAGCAGCTATTAACTGGGATAGTGGCGCACATACTATGCAAGCTCCGTG  
 180  
 CCGACCAAGGCGGTCCGAGGTCCCTTCCTCGACTCAGACATCGTCGATTAATTGACCTATACCGCGGTGTATGATACGTTCGAGGCAC  
 G W, F R Q A P G K E R E S V A A I N W D S A R T Y Y A S S V  
 1-> CDR II  
 181 AGGGGCGGATTCAACCATCTCCAGAGACAACGCCAAGAGACGGGTGTATCTGCAATGAACAGCCTGAACCTGAGGACACGGCCGTTTAT  
 270  
 TCCCGGCTAAGTGGTAGAGGTCTCTGTGGGTCTCTGCGACATAGACGTTTACTGTGCGACTTTGGACTCCTGTGCGCGGCAATA  
 R G R F T I S R D N A K K T V Y L Q M N S L K P E D T A V Y  
 1-> CDR III  
 271 ACCTGTGGCGGGGAAGGTGGTACTTGGGACTCTCTGGGGCCAGGGACCCAGGTACCGTCTCTCACAGGTGCAGTGCAGGAGTCA  
 360  
 TGGACACCGCGCCCTTCCACCATGAACCTGAGGACCCCGGTCCCTGGTCCAGTGGCAGAGGAGTGTCCACGTCGACGTCTCAGT  
 T C G A G E G G T W D S W G Q G T Q V T V S S Q V Q L Q E S  
 1-> CDR III  
 360

SUBSTITUTE SHEET (RULE 26)

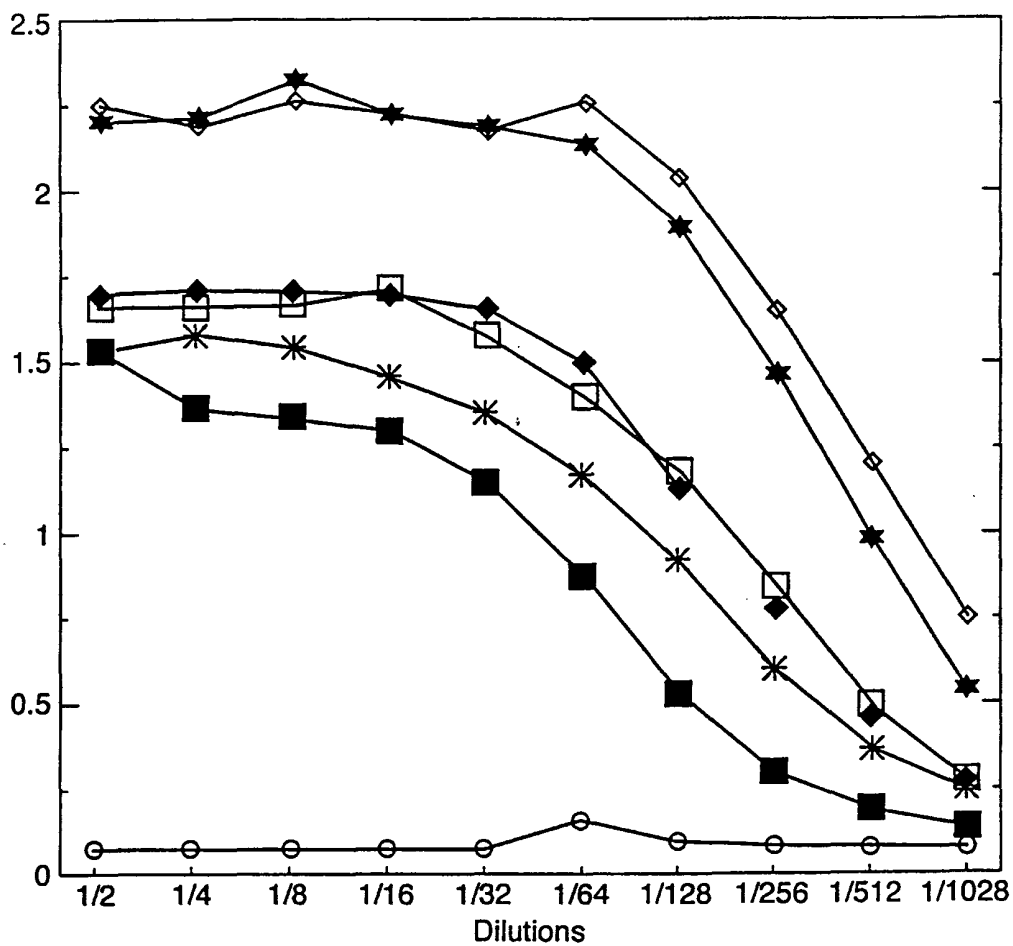
Fig.4(Cont.)

```

361      GGGGAGGCTTGGTGCAGGCTGGGAGTCTCTGAAACTCTCTGTGCAGCCTCTGGAACACCTTCACTGGCGGCTTCATGGCTGGTAC
      KpnI
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CCCCCTCGAACCACGTCGGACCCCTCAGAGACTTTGAGAGGACACGTCGGAGACCTTTGTGGAAGTCAACGCCGGAAGTACCCGACCATG
      G G G L V Q A G E S L K L S C A A S G N T F S G G F M G W Y
      1-> CDR I <-1
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
451      CGCCAGGCTCCAGGGAAGCAGCGCGAGTTGGTCGCAACCAATTAATAGAGGTATCACAACCTATGCAGACTTCGTGAAGGGCCGATTC
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      GCGGTCGGAGGTCCTTCGTGCGGCTCAACACGCGTTGGTAATTATCATCTCCATAGTGTGTTGATACGTCCTGAAGCACTTCCCGGCTAAG
      R Q A P G K Q R E L V A T I N S R G I T N Y A D F V K G R F
      1-> CDR II <-1
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
541      ACCATCTCCAGAGACAATGCCAAGAAGACAGTGTATTTGGAATGAACAGCCTGGAACCTGAAGACACGSCCGTTTATTACTGTTACACT
      EagI
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      TGGTAGAGGTCTCTGTTACGGTCTTCTGTCAATAAACCTTTACTTGTCCGACCTTGGACTTCTGTGCCGGAATAATGACAAATGTGA
      T I S R D N A K K T V Y L E M N S L E P E D T A V Y C Y T
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
631      CACTACTTCAGATCCTACTGGGTCAGGGGACCCAGGTCAAC
      BstEII
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      GTGATGAAGTCTAGGATGACCCAGTCCCTGGGTCCAGTGG
      H Y F R S Y W G Q G T Q V T
      1-> CDR III <-1
      -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
672

```

Fig.5.



pUR4619 ■  
pUR5330 ◆  
pUR5331 ★  
pUR5332 □

pUR5333 ◇  
pUR5334 ✱  
blanc ○

Fig.6.

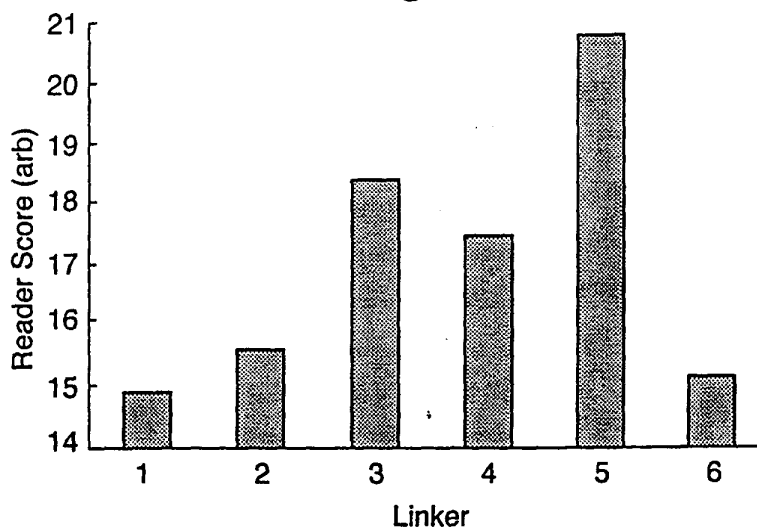


Fig.7.

